



Sequence Listing

<110> DAVID P. DAVIS
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<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR

<130> P1981R1P1-US

<140> US 10/656,598

<141> 2003-09-05

<150> US 60/410,166

<151> 2002-09-11

<160> 52

<210> 1

<211> 2470

<212> DNA

<213> Homo sapien

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 <211> 651
 <212> PRT
 <213> Homo sapien

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 35 40 45
 Thr Leu Gly Ser Asp Leu Pro Arg Ile Lys Thr Glu Ile Glu Ala
 50 55 60
 Leu Lys Asn Leu Arg His Gln His Ile Cys Gln Leu Tyr His Val
 65 70 75
 Leu Glu Thr Ala Asn Lys Ile Phe Met Val Leu Glu Tyr Cys Pro
 80 85 90
 Gly Gly Glu Leu Phe Asp Tyr Ile Ile Ser Gln Asp Arg Leu Ser
 95 100 105
 Glu Glu Glu Thr Arg Val Val Phe Arg Gln Ile Val Ser Ala Val
 110 115 120
 Ala Tyr Val His Ser Gln Gly Tyr Ala His Arg Asp Leu Lys Pro
 125 130 135
 Glu Asn Leu Leu Phe Asp Glu Tyr His Lys Leu Lys Leu Ile Asp
 140 145 150
 Phe Gly Leu Cys Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu
 155 160 165
 Gln Thr Cys Cys Gly Ser Leu Ala Tyr Ala Ala Pro Glu Leu Ile
 170 175 180
 Gln Gly Lys Ser Tyr Leu Gly Ser Glu Ala Asp Val Trp Ser Met
 185 190 195

| | | | |
|---|-----|-----|-----|
| Gly Ile Leu Leu Tyr Val Leu Met Cys Gly Phe Leu Pro Phe Asp | 200 | 205 | 210 |
| Asp Asp Asn Val Met Ala Leu Tyr Lys Lys Ile Met Arg Gly Lys | 215 | 220 | 225 |
| Tyr Asp Val Pro Lys Trp Leu Ser Pro Ser Ser Ile Leu Leu Leu | 230 | 235 | 240 |
| Gln Gln Met Leu Gln Val Asp Pro Lys Lys Arg Ile Ser Met Lys | 245 | 250 | 255 |
| Asn Leu Leu Asn His Pro Trp Ile Met Gln Asp Tyr Asn Tyr Pro | 260 | 265 | 270 |
| Val Glu Trp Gln Ser Lys Asn Pro Phe Ile His Leu Asp Asp Asp | 275 | 280 | 285 |
| Cys Val Thr Glu Leu Ser Val His His Arg Asn Asn Arg Gln Thr | 290 | 295 | 300 |
| Met Glu Asp Leu Ile Ser Leu Trp Gln Tyr Asp His Leu Thr Ala | 305 | 310 | 315 |
| Thr Tyr Leu Leu Leu Leu Ala Lys Lys Ala Arg Gly Lys Pro Val | 320 | 325 | 330 |
| Arg Leu Arg Leu Ser Ser Phe Ser Cys Gly Gln Ala Ser Ala Thr | 335 | 340 | 345 |
| Pro Phe Thr Asp Ile Lys Ser Asn Asn Trp Ser Leu Glu Asp Val | 350 | 355 | 360 |
| Thr Ala Ser Asp Lys Asn Tyr Val Ala Gly Leu Ile Asp Tyr Asp | 365 | 370 | 375 |
| Trp Cys Glu Asp Asp Leu Ser Thr Gly Ala Ala Thr Pro Arg Thr | 380 | 385 | 390 |
| Ser Gln Phe Thr Lys Tyr Trp Thr Glu Ser Asn Gly Val Glu Ser | 395 | 400 | 405 |
| Lys Ser Leu Thr Pro Ala Leu Cys Arg Thr Pro Ala Asn Lys Leu | 410 | 415 | 420 |
| Lys Asn Lys Glu Asn Val Tyr Thr Pro Lys Ser Ala Val Lys Asn | 425 | 430 | 435 |
| Glu Glu Tyr Phe Met Phe Pro Glu Pro Lys Thr Pro Val Asn Lys | 440 | 445 | 450 |
| Asn Gln His Lys Arg Glu Ile Leu Thr Thr Pro Asn Arg Tyr Thr | 455 | 460 | 465 |
| Thr Pro Ser Lys Ala Arg Asn Gln Cys Leu Lys Glu Thr Pro Ile | 470 | 475 | 480 |
| Lys Ile Pro Val Asn Ser Thr Gly Thr Asp Lys Leu Met Thr Gly | | | |

| 485 | | | | | | | | | | 490 | | | | | 495 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Val | Ile | Ser | Pro | Glu | Arg | Arg | Cys | Arg | Ser | Val | Glu | Leu | Asp | Leu | | | | | |
| | | | | 500 | | | | | 505 | | | | | 510 | | | | | |
| Asn | Gln | Ala | His | Met | Glu | Glu | Thr | Pro | Lys | Arg | Lys | Gly | Ala | Lys | | | | | |
| | | | | 515 | | | | | 520 | | | | | 525 | | | | | |
| Val | Phe | Gly | Ser | Leu | Glu | Arg | Gly | Leu | Asp | Lys | Val | Ile | Thr | Val | | | | | |
| | | | | 530 | | | | | 535 | | | | | 540 | | | | | |
| Leu | Thr | Arg | Ser | Lys | Arg | Lys | Gly | Ser | Ala | Arg | Asp | Gly | Pro | Arg | | | | | |
| | | | | 545 | | | | | 550 | | | | | 555 | | | | | |
| Arg | Leu | Lys | Leu | His | Tyr | Asn | Val | Thr | Thr | Thr | Arg | Leu | Val | Asn | | | | | |
| | | | | 560 | | | | | 565 | | | | | 570 | | | | | |
| Pro | Asp | Gln | Leu | Leu | Asn | Glu | Ile | Met | Ser | Ile | Leu | Pro | Lys | Lys | | | | | |
| | | | | 575 | | | | | 580 | | | | | 585 | | | | | |
| His | Val | Asp | Phe | Val | Gln | Lys | Gly | Tyr | Thr | Leu | Lys | Cys | Gln | Thr | | | | | |
| | | | | 590 | | | | | 595 | | | | | 600 | | | | | |
| Gln | Ser | Asp | Phe | Gly | Lys | Val | Thr | Met | Gln | Phe | Glu | Leu | Glu | Val | | | | | |
| | | | | 605 | | | | | 610 | | | | | 615 | | | | | |
| Cys | Gln | Leu | Gln | Lys | Pro | Asp | Val | Val | Gly | Ile | Arg | Arg | Gln | Arg | | | | | |
| | | | | 620 | | | | | 625 | | | | | 630 | | | | | |
| Leu | Lys | Gly | Asp | Ala | Trp | Val | Tyr | Lys | Arg | Leu | Val | Glu | Asp | Ile | | | | | |
| | | | | 635 | | | | | 640 | | | | | 645 | | | | | |
| Leu | Ser | Ser | Cys | Lys | Val | | | | | | | | | | | | | | |
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 cgtccgctgc taggaccgag gcagggctgg agctgggctg ggatcccgag 200
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 aaaaaaa 2257

<210> 4
 <211> 358
 <212> PRT
 <213> Homo sapien

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 Val Gln Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro
 35 40 45
 Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr
 50 55 60
 Ala Val Ala Thr Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu
 65 70 75
 Pro Glu Glu Gly Gly Arg Ala Tyr Gln Ala Leu His Cys Pro Thr
 80 85 90
 Gly Thr Glu Tyr Thr Cys Lys Val Tyr Pro Val Gln Glu Ala Pro
 95 100 105
 Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro Pro His Lys His Val
 110 115 120
 Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln Leu Leu Tyr Ala
 125 130 135
 Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu Val Arg Ser
 140 145 150
 Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe Arg Gln
 155 160 165
 Met Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val Leu
 170 175 180

| | | |
|-----------------|---|-------------------------|
| Arg Asp Leu Lys | Leu Cys Arg Phe Val | Phe Ala Asp Arg Glu Arg |
| 185 | | 190 195 |
| Lys Lys Leu Val | Leu Glu Asn Leu Glu Asp Ser Cys Val Leu Thr | |
| 200 | | 205 210 |
| Gly Pro Asp Asp | Ser Leu Trp Asp Lys His Ala Cys Pro Ala Tyr | |
| 215 | | 220 225 |
| Val Gly Pro Glu | Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys | |
| 230 | | 235 240 |
| Ala Ala Asp Val | Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu | |
| 245 | | 250 255 |
| Ala Gly His Tyr | Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe | |
| 260 | | 265 270 |
| Gly Lys Ile Arg | Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser | |
| 275 | | 280 285 |
| Ala Pro Ala Arg | Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro | |
| 290 | | 295 300 |
| Ala Glu Arg Leu | Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu | |
| 305 | | 310 315 |
| Arg Gln Asp Pro | Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp | |
| 320 | | 325 330 |
| Glu Ala Ala Gln | Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala | |
| 335 | | 340 345 |
| Arg Glu Glu Glu | Gly Asp Arg Glu Val Val Leu Tyr Gly | |
| 350 | | 355 |

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 <211> 1282
 <212> DNA
 <213> Homo sapien

<220>
 <221> Unsure
 <222> 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281
 <223> Unknown base

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 cacaggcaaa cccattgccc tttgagagaa agaagaggac ccggtgaaac 200
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 ctggagcagag accttcagaa gaggttcacc tgccaacagg ccttgcgagg 1000
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 ttcaatgcc a cttgttctc gcgccacatc cggaagctgg ggcagatccc 1150
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 gccttcgtgc tggccagccc cccaagtgg gatgcccagg nagatgccga 1250
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<210> 6

<211> 343

<212> PRT

<213> Homo sapien

<220>

<221> Unsure

<222> 233, 328, 333

<223> Unknown amino acid

<400> 6

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Leu | Lys | Lys | His | Thr | Glu | Asp | Ile | Ser | Ser | Val | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Arg | Glu | Arg | Leu | Gly | Ser | Gly | Ala | Phe | Ser | Glu | Val | Val |
| | | | | 20 | | | | | 25 | | | | | 30 |

Leu Ala Gln Glu Arg Gly Ser Ala His Leu Val Ala Leu Lys Cys

| | 35 | 40 | 45 |
|---|-----|-----|-----|
| Ile Pro Lys Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn | 50 | 55 | 60 |
| Glu Ile Ala Val Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala | 65 | 70 | 75 |
| Leu Glu Asp Val His Glu Ser Pro Ser His Leu Tyr Leu Ala Met | 80 | 85 | 90 |
| Glu Leu Val Thr Gly Gly Glu Leu Phe Asp Arg Ile Met Glu Arg | 95 | 100 | 105 |
| Gly Ser Tyr Thr Glu Lys Asp Ala Ser His Leu Val Gly Gln Val | 110 | 115 | 120 |
| Leu Gly Ala Val Ser Tyr Leu His Ser Leu Gly Ile Val His Arg | 125 | 130 | 135 |
| Asp Leu Lys Pro Glu Asn Leu Leu Tyr Ala Thr Pro Phe Glu Asp | 140 | 145 | 150 |
| Ser Lys Ile Met Val Ser Asp Phe Gly Leu Ser Lys Ile Gln Ala | 155 | 160 | 165 |
| Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala | 170 | 175 | 180 |
| Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala Val Asp Val | 185 | 190 | 195 |
| Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly Tyr Pro | 200 | 205 | 210 |
| Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile Leu | 215 | 220 | 225 |
| Arg Ala Ser Tyr Glu Phe Asp Xaa Pro Phe Trp Asp Asp Ile Ser | 230 | 235 | 240 |
| Glu Ser Gly Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Leu | 245 | 250 | 255 |
| Gln Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg Asp Leu Trp Ile | 260 | 265 | 270 |
| Phe Trp Asp Thr Gly Phe Gly Arg Asp Ile Leu Gly Phe Val Ser | 275 | 280 | 285 |
| Glu Gln Ile Arg Lys Asn Phe Ala Trp Thr His Trp Lys Arg Ala | 290 | 295 | 300 |
| Phe Asn Ala Thr Leu Phe Leu Arg His Ile Arg Lys Leu Gly Gln | 305 | 310 | 315 |
| Ile Pro Glu Gly Glu Gly Ala Ser Glu Gln Gly Met Xaa Arg His | 320 | 325 | 330 |

Ser His Xaa Gly Leu Arg Ala Gly Gln Pro Pro Lys Trp
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<210> 7

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Task 110 Forward primer

<400> 7

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<210> 8

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Task 110 Reverse primer

<400> 8

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<210> 9

<211> 20

<212> DNA

<213> Artificial sequence

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<223> Task 110 Probe

<400> 9

ccaggcatcg cccttaagcc 20

<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Task 119 Forward primer

<400> 10

tgccaacagt ggattgagtt 20

<210> 11

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Task 119 Reverse Primer

<400> 11

tgaaggtttg gctcagttca 20

<210> 12
<211> 24
<212> DNA
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<220>
<223> Task 119 Probe

<400> 12
tagctccaag ccttctcctg cctc 24

<210> 13
<211> 512
<212> DNA
<213> Artificial sequence

<220>
<223> Task 110 probe

<400> 13
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gacaggtgtc attagccctg agaggcggtg ccgctcagtg gaattggatc 150
tcaaccaagc acatatggag gagactccaa aaagaaaggg agccaaagtg 200
tttgggagcc ttgaaagggg gttggataag gttatcactg tgctcaccag 250
gagcaaaagg aagggttctg ccagagacgg gccagaaga ctaaagcttc 300
actataatgt gactacaact agattagtga atccagatca actgttgaat 350
gaaataatgt ctattcttcc aaagaagcat gttgactttg tacaaaaggg 400
ttatacactg aagtgtcaaa cacagtcaga ttttgggaaa gtgacaatgc 450
aatttgaatt agaagtgtgc cagcttcaaa aaccgatgt ggtgggtatc 500
aggaggcagc gg 512

<210> 14
<211> 584
<212> DNA
<213> Artificial sequence

<220>
<223> Task 119 probe

<400> 14
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cagcacggtc tggctcctgcg tgatctcaag ctgtgtcgtt ttgtcttcgc 150
tgaccgtgag aggaagaagc tgggtgctgga gaacctggag gactcctgcg 200

tgctgactgg gccagatgat tccctgtggg acaagcacgc gtgccagcc 250
 tacgtgggac ctgagatact cagctcacgg gctcatact cgggcaaggc 300
 agccgatgtc tggagcctgg gcgtggcgct cttcaccatg ctggccggcc 350
 actaccctt ccaggactcg gagcctgtcc tgctcttcgg caagatccgc 400
 cgcggggcct acgccttgcc tgcaggcctc tcggccctg cccgctgtct 450
 ggttcgctgc ctcttcgtc gggagccagc tgaacggctc acagccacag 500
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 accgattcc ctttagtgag ggttaatttc atag 584

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<220>
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 cacagcctgg ggatcgtgca ccgggacctc aagcccgaaa acctcctgta 150
 tgccacgccc tttgaggact cgaagatcat ggtctctgac tttggactct 200
 ccaaaatcca ggctgggaac atgctaggca ccgcctgtgg gacccctgga 250
 tatgtggccc cagagctctt ggagcagaaa ccctacggga aggccgtaga 300
 tgtgtggggc ctgggcgtca tctctacat cctgctgtgt gggtagccccc 350
 cttctacga cgagagcgac cctgagctct tcagccagat cctgagggcc 400
 agctatgagt ttgactctcc tttctgggat gacatctcag aatcagccaa 450
 agacttcac cggcacctc tggagcgaga cccccagaag aggttcacct 500
 gccaacaggc cttgcggcac ctttggatct ctggggacac agccttcgac 550
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<400> 16
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 <400> 17
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 <400> 18
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 <220>
 <223> SiGFP oligos - antisense

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 <220>
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 <400> 20
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 <220>
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 <400> 21
 uuggguuccc auuguuccu 19

<210> 22
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 <220>
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 <400> 22
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 <220>
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 <400> 23
 guccguuugu uaccuccua 19

 <210> 24
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 <212> DNA
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 <220>
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 <400> 24
 uacucacuac gccaaaucg 19

 <210> 25
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 <212> DNA
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 <220>
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 <400> 25
 augagugaug cgguuuagc 19

 <210> 26
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 <400> 26
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 gccugaggcu gccgugcuc 19
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 <400> 29
 cggacuccga cggcacgag 19
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 <223> siGFP siRNA oligo - sense
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 gcaagcugac ccugaaguuc au 22
 <210> 31
 <211> 22
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 <223> siGFP siRNA oligo - antisense
 <400> 31
 gccguucgac ugggacuuca ag 22
 <210> 32
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<223> siTASK120(1) siRNA oligo - sense
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 <400> 33
 ggaggacaua cggugcggg 19
 <210> 34
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 <400> 34
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 <400> 37

cgauacucuaa acugagagg 19

<210> 38
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<220>
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<400> 38
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<210> 39
 <211> 28
 <212> DNA
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<220>
 <223> TASK110(1) reverse primer

<400> 39
 ctagatagga tgtcttccac taatcttt 28

<210> 40
 <211> 20
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<220>
 <223> TASK110(1) Probe

<400> 40
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<210> 41
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<220>
 <223> TASK110(i2) Forward Primer

<400> 41
 caaagtttga gatacactat catgggtt 27

<210> 42
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<220>
 <223> TASK110(i2) reverse primer

<400> 42
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<210> 43

<211> 31
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 <400> 43
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 <210> 44
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 <220>
 <223> GAPDH forward primer

 <400> 44
 gaaggtgaag gtcggagtc 19

 <210> 45
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 <212> DNA
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 <220>
 <223> GAPDH Reverse Primer

 <400> 45
 gaagatggtg atgggatttc 20

 <210> 46
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 <400> 46
 caagcttccc gttctcagcc 20

 <210> 47
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 <220>
 <223> SPF31 Forward Primer

 <400> 47
 gcaccttagg aagccccttc 20

 <210> 48
 <211> 21
 <212> DNA
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<220>
 <223> SPF31 Reverse Primer

 <400> 48
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 <210> 49
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 <212> DNA
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 <220>
 <223> SPF 31 Probe

 <400> 49
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 <210> 50
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 <212> DNA
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 <220>
 <223> HMAD2 Forward Primer

 <400> 50
 gggtggacaa agtattaact cagatgg 27

 <210> 51
 <211> 26
 <212> DNA
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 <220>
 <223> HMAD2 Reverse Primer

 <400> 51
 gacttgattg gtgaagcttt atgaca 26

 <210> 52
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> HMAD2 Probe

 <400> 52
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